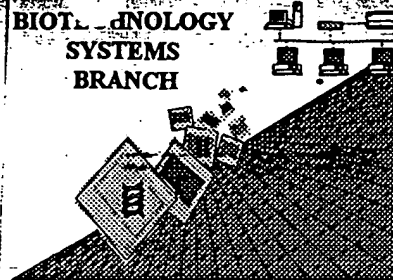


Brunner

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



DT
01-24-01

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/389,835

Source: 1647

Date Processed by STIC: 12-29-00

RECEIVED

JAN 10 2001

TECH CENTER 1600/2800

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

BEST AVAILABLE COPY **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

B. Brunner

1647

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/389,835

DATE: 12/29/2000
TIME: 13:51:20

Input Set : A:\sequence listing.txt
Output Set: N:\CRF3\12292000\I389835.raw

Does Not Comply
Corrected Diskette Needed
See PP 6, 7

5 <110> APPLICANT: Ruoho, Arnold E.
7 Geiser, Andrew H.
9 Krebs, Mark
11 Sievert, Mike
15 <120> TITLE OF INVENTION: BACTERIORHODOPSIN/G PROTEIN-COUPLED RECEPTOR CHIMERAS
20 <130> FILE REFERENCE: 960296.95581
C--> 24 <140> CURRENT APPLICATION NUMBER: US/09/389,835
C--> 26 <141> CURRENT FILING DATE: 1999-09-03
30 <150> PRIOR APPLICATION NUMBER: 60/098950
32 <151> PRIOR FILING DATE: 1998-09-03
36 <160> NUMBER OF SEQ ID NOS: 53
40 <170> SOFTWARE: PatentIn Ver. 2.0
44 <210> SEQ ID NO: 1
46 <211> LENGTH: 1626
48 <212> TYPE: DNA
50 <213> ORGANISM: Halobacterium salinarium
54 <220> FEATURE:
56 <221> NAME/KEY: CDS
58 <222> LOCATION: (394)..(1182)
62 <400> SEQUENCE: 1
64 ggatccgacg tgaagatggg gtcgccgatg ggtgcaaccg tgaagtcctg cacggctgcg 60
68 tcacgacacg agccgaccag cgacaccag aaggtgcgaa cggttgagtg ccgcaacgat 120
72 cacgagtttt tctgctgctt cgagtgttaa cgcgctgca cgcctcgact tcaccgcggg 180
76 tgtttcgaac ccagccggcc gttgaaccag caggcagcgg gcatttcaca gccgctgtgg 240
80 cccacacact cgttgggggtg cgtatttttq gtatgggttg gaatccgcgt gtcggctcgg 300
84 tgtctyacyg ttcacgtggtc taaattccgt caccagcgta ccatactgat tgggtcgtag 360
88 agttacacac atactctcgt taggtactgt tgc atg ttg gag tta ttg cca aca 414
90 Met Leu Glu Leu Leu Pro Thr
92 1 5
96 gca gtg gag ggg gta tcg cag gcc cag atc acc gga cgt ccg gag tgg 462
98 Ala Val Glu Gly Val Ser Gln Ala Gln Ile Thr Gly Arg Pro Glu Trp
100 10 15 20
104 atc tgg cta gcg ctc ggt acg gcg cta atg gga ctc ggg acg ctc tat 510
106 Ile Trp Leu Ala Leu Gly Thr Ala Leu Met Gly Leu Gly Thr Leu Tyr
108 25 30 35
112 ttc ctc gtg aaa ggg atg ggc gtc tcg gac cca gat gca aag aaa ttc 558
114 Phe Leu Val Lys Gly Met Gly Val Ser Asp Pro Asp Ala Lys Lys Phe
116 40 45 50 55
120 tac gcc atc acg acg ctc gtc cca gcc atc gcg ttc acg atg tac ctc 606
122 Tyr Ala Ile Thr Thr Leu Val Pro Ala Ile Ala Phe Thr Met Tyr Leu
124 60 65 70
128 tcg atg ctg ctg ggg tat ggc ctc aca atg gta ccg ttc ggt ggg gag 654
130 Ser Met Leu Leu Gly Tyr Gly Leu Thr Met Val Pro Phe Gly Gly Glu
132 75 80 85
136 cag aac ccc atc tac tgg gcg cgg tac gct gac tgg ctg ttc acc acg 702
138 Gln Asn Pro Ile Tyr Trp Ala Arg Tyr Ala Asp Trp Leu Phe Thr Thr
140 90 95 100

RAW SEQUENCE LISTING DATE: 12/29/2000
 PATENT APPLICATION: US/09/389,835 TIME: 13:51:20

Input Set : A:\sequence listing.txt
 Output Set: N:\CRF3\12292000\I389835.raw

```

144 ccg ctg ttg ttg tta gac ctc gcg ttg ctc gtt gac gcg gat cag gga 750
146 Pro Leu Leu Leu Leu Asp Leu Ala Leu Leu Val Asp Ala Asp Gln Gly
148 105 110 115
152 acg atc ctt gcg ctc gtc ggt gcc gac ggc atc atg atc ggg acc gcc 798
154 Thr Ile Leu Ala Leu Val Gly Ala Asp Gly Ile Met Ile Gly Thr Gly
156 120 125 130 135
160 ctg gtc ggc gca ctg acg aag gtc tac tcg tac cgc ttc qtg tqg tqg 846
162 Leu Val Gly Ala Leu Thr Lys Val Tyr Ser Tyr Arg Phe Val Trp Trp
164 140 145 150
168 gcg atc agc acc gca gcg atg ctg tac atc ctg tac gtg ctg ttc ttc 894
170 Ala Ile Ser Thr Ala Ala Met Leu Tyr Ile Leu Tyr Val Leu Phe Phe
172 155 160 165
176 ggg ttc acc tcg aag gcc gaa agc atg cgc ccc gag gtc gca tcc acg 942
178 Gly Phe Thr Ser Lys Ala Glu Ser Met Arg Pro Glu Val Ala Ser Thr
180 170 175 180
184 ttc aaa gta ctg cgt aac gtt acc gtt qtg ttg tgg tcc gcg tat ccc 990
186 Phe Lys Val Leu Arg Asn Val Thr Val Val Leu Trp Ser Ala Tyr Pro
188 185 190 195
192 gtc gtg tqg ctg atc ggc agc gaa ggt gcg gga atc gtg ccg ctg aac 1038
194 Val Val Trp Leu Ile Gly Ser Glu Gly Ala Gly Ile Val Pro Leu Asn
196 200 205 210 215
200 atc gag acg ctg ctg ttc atg gtg ctt gac gtg agc gcg aag gtc ggc 1086
202 Ile Glu Thr Leu Leu Phe Met Val Leu Asp Val Ser Ala Lys Val Gly
204 220 225 230
208 ttc ggg ctc atc ctc ctg cgc agt cgt gcg atc ttc ggc gaa gcc gaa 1134
210 Phe Gly Leu Ile Leu Leu Arg Ser Arg Ala Ile Phe Gly Glu Ala Glu
212 235 240 245
216 gcg ccg gag ccg tcc gcc ggc gac ggc gcg gcc gcg acc agc gac tga 1182
218 Ala Pro Glu Pro Ser Ala Gly Asp Gly Ala Ala Ala Thr Ser Asp
220 250 255 260
224 tcgcacacgc aggacagccc cacaaccggc gcggcttttc aacgacacac gatgagtcgc 1242
228 ccactcagtc ttgtactcgc acgatacgcg gacgacggcg acgcccagcg cgaactttcca 1302
232 gcgtcgctca acaggtcggc tgctcgtcgcg ctgcgtcgtg cggctctcgt cggtgccggc 1362
236 ggtctgttcg ccgtgccggt cctgcggtcg ttccgcatga cgttttggga agcgttcacc 1422
240 gttgtlgtg tctccgagtt cgtctcggcc atcgtggcgg cctcgcggg ctaccacctc 1482
244 tacaccacgc ccgacgacta gcagggcccg ctggcgagcc atcactcccg ctgtggcgag 1542
248 gcgacggccg ttctgtaccg ctaccgccc cccggagtcc gggacatcgg cggggcgatg 1602
252 cgcacgaac ggtaaccggc atcc 1626
258 <210> SEQ ID NO: 2
260 <211> LENGTH: 262
262 <212> TYPE: PRT
264 <213> ORGANISM: Halobacterium salinarum
268 <400> SEQUENCE: 2
270 Met Leu Glu Leu Leu Pro Thr Ala Val Glu Gly Val Ser Gln Ala Gln
272 1 5 10 15
276 Ile Thr Gly Arg Pro Glu Trp Ile Trp Leu Ala Leu Gly Thr Ala Leu
278 20 25 30
282 Met Gly Leu Gly Thr Leu Tyr Phe Leu Val Lys Gly Met Gly Val Ser
284 35 40 45

```

RAW SEQUENCE LISTING DATE: 12/29/2000
 PATENT APPLICATION: US/09/389,835 TIME: 13:51:20

Input Set : A:\sequence listing.txt
 Output Set: N:\CRF3\12292000\I389835.raw

```

288 Asp Pro Asp Ala Lys Lys Phe Tyr Ala Ile Thr Thr Leu Val Pro Ala
290      50                      55                      60
294 Ile Ala Phe Thr Met Tyr Leu Ser Met Leu Leu Gly Tyr Gly Leu Thr
296 65                      70                      75                      80
300 Met Val Pro Phe Gly Gly Glu Gln Asn Pro Ile Tyr Trp Ala Arg Tyr
302                      85                      90                      95
306 Ala Asp Trp Leu Phe Thr Thr Pro Leu Leu Leu Leu Asp Leu Ala Leu
308                      100                     105                     110
312 Leu Val Asp Ala Asp Gln Gly Thr Ile Leu Ala Leu Val Gly Ala Asp
314                      115                     120                     125
318 Gly Ile Met Ile Gly Thr Gly Leu Val Gly Ala Leu Thr Lys Val Tyr
320                      130                     135                     140
324 Ser Tyr Arg Phe Val Trp Trp Ala Ile Ser Thr Ala Ala Met Leu Tyr
326 145                     150                     155                     160
330 Ile Leu Tyr Val Leu Phe Phe Gly Phe Thr Ser Lys Ala Glu Ser Met
332                      165                     170                     175
336 Arg Pro Glu Val Ala Ser Thr Phe Lys Val Leu Arg Asn Val Thr Val
338                      180                     185                     190
342 Val Leu Trp Ser Ala Tyr Pro Val Val Trp Leu Ile Gly Ser Glu Gly
344                      195                     200                     205
348 Ala Gly Ile Val Pro Leu Asn Ile Glu Thr Leu Leu Phe Met Val Leu
350                      210                     215                     220
354 Asp Val Ser Ala Lys Val Gly Phe Gly Leu Ile Leu Leu Arg Ser Arg
356 225                     230                     235                     240
360 Ala Ile Phe Gly Glu Ala Glu Ala Pro Glu Pro Ser Ala Gly Asp Gly
362                      245                     250                     255
366 Ala Ala Ala Thr Ser Asp
368                      260
374 <210> SEQ ID NO: 3
376 <211> LENGTH: 20
378 <212> TYPE: DNA
380 <213> ORGANISM: Artificial Sequence
384 <220> FEATURE:
386 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
388     primer
392 <400> SEQUENCE: 3
394 cgcgtatcca gtcgtgtggc                                20
400 <210> SEQ ID NO: 4
402 <211> LENGTH: 20
404 <212> TYPE: DNA
406 <213> ORGANISM: Artificial Sequence
410 <220> FEATURE:
412 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
414     primer
418 <400> SEQUENCE: 4
420 cctcctgagg agtcgtgcga                                20
426 <210> SEQ ID NO: 5
428 <211> LENGTH: 91
430 <212> TYPE: DNA

```

RECEIVED
 JAN 10 2001
 TECH CENTER 1600/2900

RAW SEQUENCE LISTING DATE: 12/29/2000
 PATENT APPLICATION: US/09/389,835 TIME: 13:51:20

Input Set : A:\sequence listing.txt
 Output Set: N:\CRF3\12292000\I389835.raw

```

432 <213> ORGANISM: Artificial Sequence
436 <220> FEATURE:
438 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
440     primer
444 <400> SEQUENCE: 5
446 atcctgtacg tgctgttctt cgggttcacc gtcaaggagg cggcggcgca gcagcaggag 60
450 tcgqcgacga cgcagaaggc ggagaaggag q                               91
456 <210> SEQ ID NO: 6
458 <211> LENGTH: 96
460 <212> TYPE: DNA
462 <213> ORGANISM: Artificial Sequence
466 <220> FEATURE:
468 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
470     primer
474 <400> SEQUENCE: 6
476 cgggatacgc qgaccacaac acaacggtaa cgttacgcag tactttgaac gtggatgcga 60
480 cctccatgcg cgtgacctec ttctccgcct tctgcg                               96
486 <210> SEQ ID NO: 7
488 <211> LENGTH: 26
490 <212> TYPE: DNA
492 <213> ORGANISM: Artificial Sequence
496 <220> FEATURE:
498 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
500     primer
504 <400> SEQUENCE: 7
506 gtacatcctg tacgtgctgt tcttcg                               26
512 <210> SEQ ID NO: 8
514 <211> LENGTH: 19
516 <212> TYPE: DNA
518 <213> ORGANISM: Artificial Sequence
522 <220> FEATURE:
524 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
526     primer
530 <400> SEQUENCE: 8
532 acgacgggat acgcggacc                               19
538 <210> SEQ ID NO: 9
540 <211> LENGTH: 22
542 <212> TYPE: DNA
544 <213> ORGANISM: Artificial Sequence
548 <220> FEATURE:
550 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
552     primer
556 <400> SEQUENCE: 9
558 atcctgtacg tctgttctt cg                               22
564 <210> SEQ ID NO: 10
566 <211> LENGTH: 15
568 <212> TYPE: DNA
570 <213> ORGANISM: Artificial Sequence
574 <220> FEATURE:

```

RECEIVED
 JAN 10 2001
 TECH CENTER 1600/2900

RAW SEQUENCE LISTING DATE: 12/29/2000
 PATENT APPLICATION: US/09/389,835 TIME: 13:51:20

Input Set : A:\sequence listing.txt
 Output Set: N:\CRF3\12292000\I389835.raw

```

576 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
578     primer
582 <400> SEQUENCE: 10
584 cgggatacgc ggacc                                     15
590 <210> SEQ ID NO: 11
592 <211> LENGTH: 83
594 <212> TYPE: DNA
596 <213> ORGANISM: Artificial Sequence
600 <220> FEATURE:
602 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
604     primer
608 <400> SEQUENCE: 11
610 atcctgtacg tgcgttctt cgggttcacc gcgcgctccc acacgcgcga gatctccacg 60
614 ctcccgcgcg cgaacatgaa ggg                                     83
620 <210> SEQ ID NO: 12
622 <211> LENGTH: 75
624 <212> TYPE: DNA
626 <213> ORGANISM: Artificial Sequence
630 <220> FEATURE:
632 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
634     primer
638 <400> SEQUENCE: 12
640 cgggatacgc ggaccacaac acaacggtaa cgttacgcag tactttgaac gtggatgcga 60
644 cgcccttcat gttcg                                     75
650 <210> SEQ ID NO: 13
652 <211> LENGTH: 89
654 <212> TYPE: DNA
656 <213> ORGANISM: Artificial Sequence
660 <220> FEATURE:
662 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
664     primer
668 <400> SEQUENCE: 13
670 gggttcaccg aggtcttcta cctcatccgc aagcagctga caagaaggtc tccgcgtcct 60
674 ccgcgacccc gcagaagtac tacggcaag                                     89
680 <210> SEQ ID NO: 14
682 <211> LENGTH: 90
684 <212> TYPE: DNA
686 <213> ORGANISM: Artificial Sequence
690 <220> FEATURE:
692 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
694     primer
698 <400> SEQUENCE: 14
700 cacaacggta acgttacgca gtactttgaa cgtggatgcg acggacttcg cgatcttgag 60
704 ctecttgccg tagtacttct gcgggtcgcc                                     90
710 <210> SEQ ID NO: 15
712 <211> LENGTH: 84
714 <212> TYPE: DNA
716 <213> ORGANISM: Artificial Sequence
720 <220> FEATURE:

```

09/389,835

p.6

<210> 31

Seg # 31

<211> 87

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(90)

CDS location out of range.
Only 87 codons shown. Do
not count stop codon.

<220>

<223> Description of Artificial Sequence:chimeric loop 3
sequence

<400> 31

acc cag ctc gtc ttc acg gtc aag gag gcg gcg gcg cag cag cag gag 48

Thr Gln Leu Val Phe Thr Val Lys Glu Ala Ala Ala Gln Gln Gln Glu

1

5

10

15

tcg gcg acg acg cag aag gcg gag aag gag gtc acg gtc

87

Ser Ala Thr Thr Gln Lys Ala Glu Lys Glu Val Thr Val

20

25

RECEIVED

JAN 10 2001

TECH CENTER 1600-2900

09/389, 835

P. 7

<210> 26

Seg # 26

<211> 31

<212> PRT

<213> Artificial Sequence

Missing mandatory <220>,
<223> features to explain
source of artificial sequence.

<400> 26

Thr Gln Leu Val Phe Thr Val Lys Glu Ala Ala Ala Gln Gln Gln Glu

1

5

10

15

Ser Ala Thr Thr Gln Lys Ala Glu Lys Glu Val Thr Arg Met Val

20

25

30

This error occurs
elsewhere in the sequence
listing. Please check entire
sequence listing and correct
where necessary.

VERIFICATION SUMMARY

DATE: 12/29/2000

PATENT APPLICATION: US/09/389,835

TIME: 13:51:21

Input Set : A:\sequence listing.txt

Output Set: N:\CRF3\12292000\I389835.raw

L:24 M:270 C: Current Application Number differs, Replaced Application Number
L:26 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1050 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1050 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1122 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1122 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1200 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1200 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1236 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:31, CDS LOCATION: (1)..(90)
L:1278 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1278 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1350 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1350 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1422 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1422 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1494 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1494 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1566 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1566 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1638 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1638 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: